



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant & Gould P.C.
 - (B) STREET: P.O. Box 2903
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402-0903
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/308,830
 - (B) FILING DATE: 04-AUG-1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/22228
 - (B) FILING DATE: 05-DEC-1997
 - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/032,930
 - (B) FILING DATE: 06-DEC-1996
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Skoog, Mark T
 - (B) REGISTRATION NUMBER: 40,178
 - (C) REFERENCE/DOCKET NUMBER: 600.346USWO
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCATCACGGG TGGATTCTTG AACAGGTG

29

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATCACGCC CCCCGTCGAC GATAAAATAG TTGCTAAGCT ACAAGCT

47

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA
ATTCCATATA ATATTAATAA ATAATTAAAA AATAATAAT AAATAATTAA TC

60

120

172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA

60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAATAATAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAATAATAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAATAATAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAATAATAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCATCACGGG TGGATCCTTG AACAGGTGC A	31
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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 828...1580

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCACGCA	TCACTCATGT	TTGACAGCTT	ATCATCGATA	AGCTTACTTT	TCGAATCAGG	60
TCTATCCTTG	AAACAGGTGC	AACATAGATT	AGGGCATGGA	GATTTACCAAG	ACAACATATGA	120
ACGTATATAC	TCACATCACG	CAATCGGCAA	TTGATGACAT	TGGAACATAAA	TTCAATCAAT	180
TTGTTACTAA	CAAGCAACTA	GATTGACAAC	TAATTCTCAA	CAAACGTAA	TTAACAAACA	240
TTCAAGTAAC	TCCCACCCAGC	TCCATCAATG	CTTACCGTAA	GTAATCATAA	CTTACTAAAAA	300
CCTTGTACA	TCAAGGTTTT	TTCTTTTGT	CTTGTTCATG	AGTTACCATATA	ACTTTCTATA	360
TTATTGACAA	CTAAATTGAC	AACTCTCAA	TTATTTTCT	GTCTACTCAA	AGTTTCTTC	420
ATTTGATATA	GTCTAATTCC	ACCATCACTT	CTTCCACTCT	CTCTACCGTC	ACAACTTCAT	480
CATCTCTCAC	TTTTCTGTGT	GGTAACACAT	AATCAAATAT	CTTCCGTTT	TTACGCACATA	540
TCGCTACTGT	GTCACCTAAA	ATATACCCCT	TATCAATCGC	TTCTTTAAC	TCATCTATAT	600
ATAACATATT	TCATCCTCCT	ACCTATCTAT	TCGTAAAAAG	ATAAAAATAA	CTATTGTTTT	660
TTTTGTTATT	TTATAATAAA	ATTATTAATA	TAAGTTAATG	TTTTTTAAAA	ATATACAATT	720
TTATTCTATT	TATAGTTAGC	TATTTTTCA	TTGTTAGTAA	TATTGGTGAA	TTGTAATAAC	780
CTTTTAAAT	CTAGAGGAGA	ACCCAGATAT	AAAATGGAGG	AATATTA	ATG GAA AAC	836
				Met	Glu Asn	
				1		
AAT AAA AAA	GTA TTG AAG AAA	ATG GTA TTT	TTT GTT TTA	GTG ACA TTT		884
Asn Lys Lys	Val Leu Lys Lys	Met Val Phe	Phe Val Leu Val	Thr Phe		
5	10	15				
CTT GGA CTA ACA ATC TCG CAA GAG GTA TTT GCT	CAA CAA GAC CCC GAT					932
Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala	Gln Gln Asp Pro Asp					
20	25	30	35			
CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT CAA AAT ATA						980
Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile						
40	45	50				
TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT						1028
Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser						
55	60	65				
GTT GAT CAA CTT TTA TCT CAC CAT TTA ATA TAT AAT GTT TCA GGG CCA						1076
Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro						
70	75	80				
AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT						1124

Asn	Tyr	Asp	Lys	Leu	Lys	Thr	Glu	Leu	Lys	Asn	Gln	Glu	Met	Ala	Thr	
85																95
TTA	TTT	AAG	GAT	AAA	AAC	GTT	GAT	ATT	TAT	GGT	GTA	GAA	TAT	TAC	CAT	1172
Leu	Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	Val	Glu	Tyr	Tyr	His	
100																115
CTC	TGT	TAT	TTA	TGT	GAA	AAT	GCA	GAA	AGG	AGT	GCA	TGT	ATC	TAC	GGA	1220
Leu	Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys	Ile	Tyr	Gly	
120																125
GGG	GTA	ACA	AAT	CAT	GAA	GGG	AAT	CAT	TTA	GAA	ATT	CCT	AAA	AAG	ATA	1268
Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His	Leu	Glu	Ile	Pro	Lys	Lys	Ile	
135																140
GTC	GTT	AAA	GTA	TCA	ATC	GAT	GGT	ATC	CAA	AGC	CTA	TCA	TTT	GAT	ATT	1316
Val	Val	Lys	Val	Ser	Ile	Asp	Gly	Ile	Gln	Ser	Leu	Ser	Phe	Asp	Ile	
150																155
165																170
GAA	ACA	AAT	AAA	AAA	ATG	GTA	ACT	GCT	CAA	GAA	TTA	GAC	TAT	AAA	GTT	1364
Glu	Thr	Asn	Lys	Lys	Met	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Lys	Val	
175																
AGA	AAA	TAT	CTT	ACA	GAT	AAT	AAG	CAA	CTA	TAT	ACT	AAT	GGA	CCT	TCT	1412
Arg	Lys	Tyr	Leu	Thr	Asp	Asn	Lys	Gln	Leu	Tyr	Thr	Asn	Gly	Pro	Ser	
180																185
190																195
AAA	TAT	GAA	ACT	GGA	TAT	ATA	AAG	TTC	ATA	CCT	AAG	AAT	AAA	GAA	AGT	1460
Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Pro	Lys	Asn	Lys	Glu	Ser	
200																205
210																
TTT	TGG	TTT	GAT	TTT	TTC	CCT	GAA	CCA	GAA	TTT	ACT	CAA	TCT	AAA	TAT	1508
Phe	Trp	Phe	Asp	Phe	Pro	Glu	Pro	Glu	Phe	Thr	Gln	Ser	Lys	Tyr		
215																220
225																
CTT	ATG	ATA	TAT	AAA	GAT	AAT	GAA	ACG	CTT	GAC	TCA	AAC	ACA	AGC	CAA	1556
Leu	Met	Ile	Tyr	Lys	Asp	Asn	Glu	Thr	Leu	Asp	Ser	Asn	Thr	Ser	Gln	
230																235
240																
ATT	GAA	GTC	TAC	CTA	ACA	ACC	AAG	TAAC	TTTTG	CTTTGGCAA	CCTTACCTAC					1610
Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys									
245																250
TGCTGGATT	TT	AGAAATTTA	TTGCAATTCT	TTTATTAATG	TT	AAAAACCGC	TCATTTGATG									1670
AGCGGTTTG	TCTTATCTAA	AGGAGCTTAA	CCTCTTAATG	CTGAAAATT	TTAAATGTTG											1730
GATTTTTGTA	TTTGCTATT	GTATTTGATG	GGTAATCCC	TTTTTCGACA	GACATCGTCG											1790
TGCCACCTCT	AACACCAAAA	TCATAGACAG	GAGCTTGTAG	CTTAGCAACT	ATTTTATCGT											1850
C																1851

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Glu Asn Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu
1 5 10 15
Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln
20 25 30
Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
35 40 45
Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
50 55 60
Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
65 70 75 80
Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
85 90 95
Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
100 105 110
Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
115 120 125
Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
130 135 140
Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
145 150 155 160
Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
165 170 175
Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
180 185 190
Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
195 200 205
Lys Glu Ser Phe Trp Phe Asp Phe Pro Glu Pro Glu Phe Thr Gln
210 215 220
Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
225 230 235 240
Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
245 250